

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,434  
Source: IFWO  
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## RAW SEQUENCE LISTING

DATE: 08/25/2006

PATENT APPLICATION: US/10/538,434

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3 <110> APPLICANT: Jahn, Margaret M.
4   Kang, Byoung-Cheorl
6 <120> TITLE OF INVENTION: RECESSIVE PLANT VIRAL RESISTANCE RESULTS FROM MUTATIONS
7   IN TRANSLATION INITIATION FACTOR eIF4E
9 <130> FILE REFERENCE: 19603/4252
11 <140> CURRENT APPLICATION NUMBER: 10/538,434
C--> 12 <141> CURRENT FILING DATE: 2005-06-10
14 <150> PRIOR APPLICATION NUMBER: 60/434,220
15 <151> PRIOR FILING DATE: 2002-12-17
17 <150> PRIOR APPLICATION NUMBER: PCT/US03/40184
18 <151> PRIOR FILING DATE: 2003-12-17
20 <160> NUMBER OF SEQ ID NOS: 39
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 875
26 <212> TYPE: DNA
27 <213> ORGANISM: Capsicum annuum
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32 aggtgaaatt gttgaagaaa ctgatgatac gacgtcgtat ttgagcaaag aaatagcaac 180
33 aaagcatcca ttagagcatt catggacttt ctggtttgat aatccagtgg cgaaatcgaa 240
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35 ttggggtgct tacaataata tccaccaccc aagcaagtta gttgtgggag cagacttaca 360
36 ttgtttcaag cataaaattg agccaaagtg ggaagatcct gtatgtgcca atggagggac 420
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41 tcacgacgat gcaaagaggc tcgacagaaa tgcaaagaat cgttacacag tataattctt 720
42 gatgcaatgt cggaatataa gaaacacaat tcgtactgaa aagttgtagg cactagttta 780
43 gtttctcata cgataaagct tctggtttga gtacctgtg tattggtgtt tgcactttct 840
44 aatcgcgtaa aattgtccgg ttttgatttc aaaaa 875
47 <210> SEQ ID NO: 2
48 <211> LENGTH: 228
49 <212> TYPE: PRT
50 <213> ORGANISM: Capsicum annuum
52 <400> SEQUENCE: 2
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56 Lys Val Lys Leu Asn Ala Asn Glu Ala Asp Asp Glu Val Glu Glu Gly
57   20           25           30
59 Glu Ile Val Glu Glu Thr Asp Asp Thr Thr Ser Tyr Leu Ser Lys Glu

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60          35          40          45
62 Ile Ala Thr Lys His Pro Leu Glu His Ser Trp Thr Phe Trp Phe Asp
63          50          55          60
65 Asn Pro Val Ala Lys Ser Lys Gln Ala Ala Trp Gly Ser Ser Leu Arg
66 65          70          75          80
68 Asn Val Tyr Thr Phe Ser Thr Val Glu Asp Phe Trp Gly Ala Tyr Asn
69          85          90          95
71 Asn Ile His His Pro Ser Lys Leu Val Val Gly Ala Asp Leu His Cys
72          100          105          110
74 Phe Lys His Lys Ile Glu Pro Lys Trp Glu Asp Pro Val Cys Ala Asn
75          115          120          125
77 Gly Gly Thr Trp Lys Met Ser Phe Ser Lys Gly Lys Ser Asp Thr Ser
78          130          135          140
80 Trp Leu Tyr Thr Leu Leu Ala Met Ile Gly His Gln Phe Asp His Glu
81 145          150          155          160
83 Asp Glu Ile Cys Gly Ala Val Val Ser Val Arg Gly Lys Gly Glu Lys
84          165          170          175
86 Ile Ser Leu Trp Thr Lys Asn Ala Ala Asn Glu Thr Ala Gln Val Ser
87          180          185          190
89 Ile Gly Lys Gln Trp Lys Gln Phe Leu Asp Tyr Ser Asp Ser Val Gly
90          195          200          205
92 Phe Ile Phe His Asp Asp Ala Lys Arg Leu Asp Arg Asn Ala Lys Asn
93          210          215          220
95 Arg Tyr Thr Val
96 225

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99 &lt;210&gt; SEQ ID NO: 3

100 &lt;211&gt; LENGTH: 687

101 &lt;212&gt; TYPE: DNA

102 &lt;213&gt; ORGANISM: Capsicum chinense

104 &lt;400&gt; SEQUENCE: 3

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107 acgacgtcgt atttgagcaa agaaatagca gcaaagcatc cattagagca ttcattggact 180
108 ttctggtttg ataatacagt ggcgaaatcg agacaagctg cttggggtag ctcgcttcgc 240
109 aacgtctaca ctttctccac tggtgaagat ttttggggtg cttacaataa tatccaccac 300
110 ccaagcaagt tagttgtgag agcagactta cattgtttca agcataaaat tgagccaaaag 360
111 tgggaagatc ctgtatgtgc caatggaggg acatggaaaa tgagtttttc aaagggtaaa 420
112 tctgatacca gctggctata tacgctgctt gcaatgattg gacatcaatt cgatcatgaa 480
113 gatgaaattt gtggagcagt agttagtgtc agaggtaagg gagaaaaaat atctttgtgg 540
114 accaagaatg ctgcaaatga aacggctcag gtttagcattg gtaagcaatg gaagcagttt 600
115 ctggattaca gcgacagtgt tggcttcata tttcacgacg atgcaaagag gctcgacaga 660
116 aatgcaaaga atcgttacac cgtatag 687

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119 &lt;210&gt; SEQ ID NO: 4

120 &lt;211&gt; LENGTH: 228

121 &lt;212&gt; TYPE: PRT

122 &lt;213&gt; ORGANISM: Capsicum chinense

124 &lt;400&gt; SEQUENCE: 4

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125 Met Ala Thr Ala Glu Met Glu Lys Thr Thr Thr Phe Asp Glu Ala Glu
126 1          5          10          15

```

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128 Lys Val Lys Leu Asn Ala Asn Glu Ala Asp Asp Glu Val Glu Glu Gly
129           20           25           30
131 Glu Ile Val Glu Glu Thr Asp Asp Thr Thr Ser Tyr Leu Ser Lys Glu
132           35           40           45
134 Ile Ala Ala Lys His Pro Leu Glu His Ser Trp Thr Phe Trp Phe Asp
135           50           55           60
137 Asn Thr Val Ala Lys Ser Arg Gln Ala Ala Trp Gly Ser Ser Leu Arg
138 65           70           75           80
140 Asn Val Tyr Thr Phe Ser Thr Val Glu Asp Phe Trp Gly Ala Tyr Asn
141           85           90           95
143 Asn Ile His His Pro Ser Lys Leu Val Val Arg Ala Asp Leu His Cys
144           100          105          110
146 Phe Lys His Lys Ile Glu Pro Lys Trp Glu Asp Pro Val Cys Ala Asn
147           115          120          125
149 Gly Gly Thr Trp Lys Met Ser Phe Ser Lys Gly Lys Ser Asp Thr Ser
150           130          135          140
152 Trp Leu Tyr Thr Leu Leu Ala Met Ile Gly His Gln Phe Asp His Glu
153 145           150          155          160
155 Asp Glu Ile Cys Gly Ala Val Val Ser Val Arg Gly Lys Gly Glu Lys
156           165          170          175
158 Ile Ser Leu Trp Thr Lys Asn Ala Ala Asn Glu Thr Ala Gln Val Ser
159           180          185          190
161 Ile Gly Lys Gln Trp Lys Gln Phe Leu Asp Tyr Ser Asp Ser Val Gly
162           195          200          205
164 Phe Ile Phe His Asp Asp Ala Lys Arg Leu Asp Arg Asn Ala Lys Asn
165           210          215          220
167 Arg Tyr Thr Val
168 225

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171 &lt;210&gt; SEQ ID NO: 5

172 &lt;211&gt; LENGTH: 687

173 &lt;212&gt; TYPE: DNA

174 &lt;213&gt; ORGANISM: Capsicum annuum

176 &lt;400&gt; SEQUENCE: 5

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178 aatgctaatag aggcagatga tgaagttgaa gaaggtgaaa ttgttgaaga aactgatgat 120
179 acgacgtcgt atttgagcaa agaaatagca acaaagcatc cattagagca ttcacggact 180
180 ttctggtttg ataatccaga ggcgaaatcg aaacaagctg cttggggtag ctgcgctcgc 240
181 aacgtctaca ctttctccac tgttgaagat ttttggggtg cttacaataa tatccaccac 300
182 ccaagcaagt tagttgtggg agcagactta cattgtttca agcataaaat tgagccaaaag 360
183 tgggaagatc ctgtatgtgc caatggaggg acatggaaaa tgagtttttc aaagggtaaa 420
184 tctgatacca gctggctata tacgctgctt gcaatgattg gacatcaatt cgatcatgaa 480
185 gatgaaatth gtggagcagt agttagtgtc agaggttaagg gagaaaaaat atctttgtgg 540
186 accaagaatg ctgcaaatga aacggctcag gtttagcattg gtaagcaatg gaagcagttt 600
187 ctggattaca gcgacagtgt tggcttcata ttccacgacg atgcaaagag gctcgacaga 660
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191 &lt;210&gt; SEQ ID NO: 6

192 &lt;211&gt; LENGTH: 228

193 &lt;212&gt; TYPE: PRT

194 &lt;213&gt; ORGANISM: Capsicum annuum

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## 196 &lt;400&gt; SEQUENCE: 6

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197 Met Ala Thr Ala Glu Met Glu Lys Thr Thr Thr Phe Asp Glu Ala Glu
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200 Lys Val Lys Leu Asn Ala Asn Glu Ala Asp Asp Glu Val Glu Glu Gly
201           20           25           30
203 Glu Ile Val Glu Glu Thr Asp Asp Thr Thr Ser Tyr Leu Ser Lys Glu
204           35           40           45
206 Ile Ala Thr Lys His Pro Leu Glu His Ser Trp Thr Phe Trp Phe Asp
207           50           55           60
209 Asn Pro Glu Ala Lys Ser Lys Gln Ala Ala Trp Gly Ser Ser Arg Arg
210           65           70           75           80
212 Asn Val Tyr Thr Phe Ser Thr Val Glu Asp Phe Trp Gly Ala Tyr Asn
213           85           90           95
215 Asn Ile His His Pro Ser Lys Leu Val Val Gly Ala Asp Leu His Cys
216           100          105          110
218 Phe Lys His Lys Ile Glu Pro Lys Trp Glu Asp Pro Val Cys Ala Asn
219           115          120          125
221 Gly Gly Thr Trp Lys Met Ser Phe Ser Lys Gly Lys Ser Asp Thr Ser
222           130          135          140
224 Trp Leu Tyr Thr Leu Leu Ala Met Ile Gly His Gln Phe Asp His Glu
225          145          150          155          160
227 Asp Glu Ile Cys Gly Ala Val Val Ser Val Arg Gly Lys Gly Glu Lys
228           165          170          175
230 Ile Ser Leu Trp Thr Lys Asn Ala Ala Asn Glu Thr Ala Gln Val Ser
231           180          185          190
233 Ile Gly Lys Gln Trp Lys Gln Phe Leu Asp Tyr Ser Asp Ser Val Gly
234           195          200          205
236 Phe Ile Phe His Asp Asp Ala Lys Arg Leu Asp Arg Asn Ala Lys Asn
237           210          215          220
239 Arg Tyr Thr Val
240 225

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243 &lt;210&gt; SEQ ID NO: 7

244 &lt;211&gt; LENGTH: 687

245 &lt;212&gt; TYPE: DNA

246 &lt;213&gt; ORGANISM: Capsicum annuum

## 248 &lt;400&gt; SEQUENCE: 7

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250 aatgctaatag aggcagatga tgaagttaa gaagtgaaa ttgttgaaga aactgatgat 120
251 acgacgtcgt atttgagcaa agaaatagca acaaagcatc cattagagca ttcattggact 180
252 ttctggtttg ataatccaga ggcgaaatcg aaacaagctg cttggggtag ctcgcgtcgc 240
253 aacgtctaca ctttctccac tgttgaagat ttttgggggtg cttacaataa tatccaccac 300
254 ccaagcaagt tagttgtggg agcaaactta cattgtttca agcataaaat tgagccaaag 360
255 tgggaagatc ctgtatgtgc caatggaggg acatggaaaa tgagtttttc aaagggtaaa 420
256 tctgatacca gctggctata tacgctgctt gcaatgattg gacatcaatt cgatcatgaa 480
257 gatgaaattt gtggagcagt agttagtgtc agaggtaagg gagaaaaaat atctttgtgg 540
258 accaagaatg ctgcaaataa aacggctcag gtttagcattg gtaagcaatg gaagcagttt 600
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260 aatgccaaga atcgttacac cgtatag
261                                     687
263 <210> SEQ ID NO: 8

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264 &lt;211&gt; LENGTH: 228

265 &lt;212&gt; TYPE: PRT

266 &lt;213&gt; ORGANISM: Capsicum annuum

268 &lt;400&gt; SEQUENCE: 8

269 Met Ala Thr Ala Glu Met Glu Lys Thr Thr Thr Phe Asp Glu Ala Glu

270 1 5 10 15

272 Lys Val Lys Leu Asn Ala Asn Glu Ala Asp Asp Glu Val Glu Gly

273 20 25 30

275 Glu Ile Val Glu Glu Thr Asp Asp Thr Thr Ser Tyr Leu Ser Lys Glu

276 35 40 45

278 Ile Ala Thr Lys His Pro Leu Glu His Ser Trp Thr Phe Trp Phe Asp

279 50 55 60

281 Asn Pro Glu Ala Lys Ser Lys Gln Ala Ala Trp Gly Ser Ser Arg Arg

282 65 70 75 80

284 Asn Val Tyr Thr Phe Ser Thr Val Glu Asp Phe Trp Gly Ala Tyr Asn

285 85 90 95

287 Asn Ile His His Pro Ser Lys Leu Val Val Gly Ala Asn Leu His Cys

288 100 105 110

290 Phe Lys His Lys Ile Glu Pro Lys Trp Glu Asp Pro Val Cys Ala Asn

291 115 120 125

293 Gly Gly Thr Trp Lys Met Ser Phe Ser Lys Gly Lys Ser Asp Thr Ser

294 130 135 140

296 Trp Leu Tyr Thr Leu Leu Ala Met Ile Gly His Gln Phe Asp His Glu

297 145 150 155 160

299 Asp Glu Ile Cys Gly Ala Val Val Ser Val Arg Gly Lys Gly Glu Lys

300 165 170 175

302 Ile Ser Leu Trp Thr Lys Asn Ala Ala Asn Glu Thr Ala Gln Val Ser

303 180 185 190

305 Ile Gly Lys Gln Trp Lys Gln Phe Leu Asp Tyr Ser Asp Ser Val Gly

306 195 200 205

308 Phe Ile Phe His Asp Asp Ala Lys Arg Leu Asp Arg Asn Ala Lys Asn

309 210 215 220

311 Arg Tyr Thr Val

312 225

315 &lt;210&gt; SEQ ID NO: 9

316 &lt;211&gt; LENGTH: 19

317 &lt;212&gt; TYPE: DNA

318 &lt;213&gt; ORGANISM: Artificial Sequence

320 &lt;220&gt; FEATURE:

321 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Primer

323 &lt;400&gt; SEQUENCE: 9

324 atggcaacag ctgaaatgg 19

327 &lt;210&gt; SEQ ID NO: 10

328 &lt;211&gt; LENGTH: 24

329 &lt;212&gt; TYPE: DNA

330 &lt;213&gt; ORGANISM: Artificial Sequence

332 &lt;220&gt; FEATURE:

333 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Primer

335 &lt;400&gt; SEQUENCE: 10

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